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(54) Title: PROSTATE SPECIFIC ANTIGEN SUBSTRATES (57) Abstract The present invention relates to improved prostate specific antigen substrates, and provides for a method of purifying such substrates as well as compositions comprising the substrates themselves. These substrates may be used in assays which measure prostate specific antigen activity. Such assays may provide a clinical evaluation of patients suffering from, or at risk for, prostate cancer, and also may be used to identify therapeutically useful inhibitors of prostate specific antigen activity.		

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PROSTATE SPECIFIC ANTIGEN SUBSTRATES

Description

1. Introduction

The present invention relates to improved prostate specific antigen substrates, and provides for a method of identifying such substrates as well as compositions comprising the substrates themselves. These substrates may be used in assays which measure prostate specific antigen activity. Such assays may provide a clinical evaluation of patients suffering from, or at risk for, prostate cancer, and also may be used to identify therapeutically useful inhibitors of prostate specific antigen activity.

2. Background Of The Invention

Prostate specific antigen ("PSA") is produced by the prostatic epithelium and constitutes a major component of seminal plasma, where it is found at a concentration of about 1.0 mg/ml (Webber et al., 1995, Clin. Cancer Res. 1:1089-1094). In its normal physiologic function, PSA liquefies coagulated seminal plasma approximately 20 minutes after ejaculation (*Id.*). Absent aberrant histology, PSA secretion occurs at the apical, luminal surface of the prostatic epithelium. However, when the orientation of the epithelial cells becomes disorganized (e.g., in prostate carcinoma), PSA is secreted into surrounding tissues. As a result, PSA enters the bloodstream; its presence in serum, at elevated levels, is widely used as a marker of prostate disease.

It has been estimated that serum PSA measurement can detect twice as many prostate cancers as digital rectal examination (Kardamakis, 1996, Anticancer Res. 16:2285-2288; Catalona et al., 1991, N. Engl. J. Med. 324:1156-1161). Considering that prostate cancer is the most common malignancy in adult men, with more than 200,000 new cases of prostate cancer occurring in the United States each year, the diagnostic and prognostic measurement of PSA, initiated in 1986, is now widely implemented (*Id.*, Huncharek and Muscat, 1996, Abdominal Imaging 21:364-367; Scher et

al., 1994, Seminars in Oncol. 21:630-656; Lee et al., 1995, J. Clin. Oncol. 13:464-469; Zelefsky et al., 1995, J. Clin. Oncol. 13:459-463). Such uses of PSA are not without limitations; PSA is sometimes unreliable in differentiating between benign and malignant prostate disease, especially when the serum
5 PSA level is only slightly elevated (McCormack et al., 1995, Urology 45:729-744).

Chemically, PSA is a single chain glycoprotein having a molecular weight of approximately 33,000 (Wang et al., 1982, Methods Cancer Res. 19:179-197; Webber et al., 1995, Clin. Cancer Res. 1:1089-
10 1094). cDNA and genomic DNA encoding human PSA have been cloned and sequenced (Lundwall and Lilja, 1987, FEBS Let. 214:317-322; Schulz et al., 1988, Nucl. Acids Res. 16:6226; Klobeck et al., 1989, Nucl. Acids Res. 17:3981). In terms of its functional activity, PSA is a serine protease enzyme and is now known to be a member of the human tissue kallikrein gene family
15 (McCormack et al., 1995, Urology 45:729-744; Lundwall, 1989, Biochem. Biophys. Res. Comm. 161:1151-1159; Henttu and Vihko, 1989, Biochem. Biophys. Res. Comm. 160:903-910; kallikreins were originally defined as proteases that cleave vasoactive peptides (*i.e.*, kinins) from kininogen). Like
20 In its normal function, PSA degrades the seminal fluid proteins semenogelin and fibronectin during liquefaction (Webber et al., 1995, Clin. Cancer Res. 1:1089-1094).

It has been suggested that PSA may facilitate human prostate cancer cell invasion (*Id.*; Peehl, 1995, Cancer Suppl. 75:2021-2026).
25 Circulating PSA-positive cells have been observed to correlate with metastatic prostate cancer (Hamdy et al., 1992, Br. J. Urol. 69:392-396). Furthermore, it is known that certain receptors controlling cell growth become oncogenes when their extracellular domains are removed, and it has recently been found that PSA cleaves insulin-like growth factor binding protein-3 (Cohen et al.,
30 1992, J. Clin. Endocrinol. Metab. 76:1046-1053). Monoclonal antibodies directed toward PSA inhibited invasion of reconstituted basement membrane by prostate cancer cells *in vitro*. These studies were, however, unable to

evaluate the role of other proteases (including PSA-homologous proteases) or the actual function of PSA *in vivo*. Interestingly, the major immunodetectable form of PSA in serum is a complex in which PSA is covalently bound to α_1 -antichymotrypsin inhibitor (McCormack et al., 1995, Urology 45:729-744). The other major form is free PSA (*Id.*). Further, elevated PSA levels have recently been detected in breast cancers in women; in this setting, high PSA levels are reportedly associated with low malignant potential (Yu et al., 1995, Cancer Res. 55:2104-2110).

3. Summary Of The Invention

The present invention relates to improved prostate specific antigen substrates, and provides for a method of identifying such substrates as well as compositions comprising the substrates themselves. It is based, at least in part, on the discovery that a phage display library, exhibiting random hexameric peptides, could be used to identify PSA peptide substrates. By selecting for peptides with enhanced cleavage kinetics and/or better specificity relative to known PSA substrates, the present invention may be used to identify PSA substrates which may be used advantageously in efficient assays of PSA activity which screen for potential PSA inhibitors. These assays may also be used clinically to determine the amount of active, as compared to inactive, PSA in patient serum. Such activity may bear a positive correlation with the malignant potential of a patient's prostate disease, and may be used to establish effective levels of therapeutic agents.

4. Description Of The Figures

FIGURE 1 depicts amino acids occurring at position 1 of test substrate hexameric peptide.

FIGURE 2 depicts amino acids occurring at position 2 of test substrate hexameric peptide.

FIGURE 3 depicts amino acids occurring at position 3 of test substrate hexameric peptide.

FIGURE 4 depicts amino acids occurring at position 4 of test substrate hexameric peptide.

FIGURE 5 depicts amino acids occurring at position 5 of test substrate hexameric peptide.

5 FIGURE 6 depicts amino acids occurring at position 6 of test substrate hexameric peptide.

FIGURE 7 depicts specific test substrates (SEQ ID NOS:2-80) corresponding to consensus peptide LYSGDA (SEQ ID NO:1).

10 FIGURE 8 depicts specific test substrates (SEQ ID NOS:82-109) corresponding to consensus peptide LYSGDV(SEQ ID NO:81).

FIGURE 9 depicts specific test substrates (SEQ ID NOS:111-119) corresponding to consensus peptide LYAGSE (SEQ ID NO:110).

FIGURE 10 depicts specific test substrates (SEQ ID NOS:121-134) corresponding to consensus peptide LYSGDT(SEQ ID NO:120).

15 FIGURE 11 depicts specific test substrates (SEQ ID NOS:136-165) corresponding to consensus peptide YYSGRA (SEQ ID NO:135).

FIGURE 12 depicts specific test substrates (SEQ ID NOS:167-177) corresponding to consensus peptide KRGRKK (SEQ ID NO:166).

20 FIGURE 13 depicts specific test substrates (SEQ ID NOS:179-197) corresponding to consensus peptide LNSRGN (SEQ ID NO:178).

FIGURE 14A-C depict analysis of purity of PSA in FPLC fractions of final PSA purification steps, by (A) silver stain; (B) western blot; and (C) casein substrate gel.

25 FIGURE 15A-E depict the use of a dot blot assay for scoring the ability of PSA to cleave substrate expressed by phage; successive panels A->E reflect increasing cleavage by PSA. Each panel depicts the results of duplicate experiments; moving from top to bottom in each column of dots reflects increased incubation time, in particular 0 min., 30 min., 90 min. and 150 min.

FIGURE 16A-G depict the time course of peptide cleavage at a 1:100 molar PSA:peptide ratio, using fluorescence as an index of cleavage over indicated time intervals. Scores are determined as set forth in Figure 15.

FIGURE 17A-B depict a comparison of the cleavage activity of (A) recombinant PSA versus (B) naturally occurring PSA. The same amount of peptide MR2, a concentration of 20 μ M, was used as the substrate in both sets of experiments. Cleavage was quantified by measuring fluorescence. From this data, it was estimated that recombinant PSA is more than 100 times more efficient at cleaving MR2 peptide than natural PSA.

FIGURE 18 depicts lists of peptides cleaved by 250 μ g/ml PSA (Series B; SEQ ID NOS:198-281) and 50 μ g/ml PSA (Series C; SEQ ID NOS:282-321).

5. Detailed Description Of The Invention

For purposes of clarity of description, and not by way of limitation, the detailed description of the invention has been divided into the following subsections: (a) methods of identifying PSA substrates; (b) PSA substrate compositions; and (c) uses of PSA substrates.

5.1 Methods For Purifying PSA Substrates

The present invention provides for methods of identifying improved PSA substrates which comprise exposing a peptide display clonal library to active PSA and then selecting clones which display peptides cleaved by PSA. Those peptides which are determined to be cleaved by PSA may then be subjected to further evaluation to determine the kinetics of PSA cleavage. Peptide substrates exhibiting favorable kinetics may then be selected for further use.

The term "PSA", as used herein, refers to human PSA. PSA may be prepared from natural sources or may, alternatively, be recombinantly expressed (see example section 6, *infra*).

The term "PSA substrate", as used herein, refers to peptide substrates identified by the method set forth in this section, as well as larger molecules comprising such peptide substrates (see below).

The term "peptide display clonal library", as used herein, refers to a collection of clones which encode in their nucleic acid and express as protein a variety of peptide sequences (hereafter, "test substrates"). The test substrates are expressed in a manner which is accessible to exogenously added PSA. For example, filamentous bacteriophage-based peptide libraries, as described in Smith et al., 1995, J. Biological Chem. 270:6440-6449; Matthews and Wells, 1993, Science 260:1113-1117; Hoess, 1993, Curr. Opin. Struct. Biol. 3:572-579; and Scott, 1992, Trends Biochem. Sci. 17:241-245, may be used according to the invention for this purpose. The test substrates may be peptides of any length accommodated by the vector organism, but may preferably be about 6-10 amino acids in length.

Selection of clones which express a peptide substrate of PSA may be identified by affinity binding techniques. For example, members of a phage display library may express a protein comprising test substrate as well as one member of an affinity binding pair. The configuration of test substrate and affinity binding member may be such that cleavage of the test substrate may release the affinity binding member from the phage; phage lacking the affinity binding member (and therefore encoding true PSA substrate) would fail to bind to an affinity column containing the other member of the affinity binding pair, permitting the selection of clones encoding true PSA peptide substrate. Conversely, cleavage of test substrate could be designed to unmask a member of an affinity binding pair, so that clones encoding true substrate would be retained by the corresponding affinity column.

For example, a library such as the fAFF-TC-LIB-N₆ library, as described in Smith et al., 1995, J. Biol. Chem. 270:6440-6449, may be used. This library was prepared from the fd-derived plasmid fAFF-1; phage express test substrate comprised in the amino-terminal region of the display protein pIII, as well as a "tether" peptide added to the pIII amino terminus. Degenerate oligonucleotides (5'-CAGMNNMNNMNNMNNMNNMNNACCCTACCACCGC-3' (SEQ ID NO:322), where N is A,C,T,G (equimolar) and M is C or A (equimolar)) were used to create the test substrate-encoding region. The tether is a peptide

sequence that enables attachment of the phage through binding of the tether sequence to an immobile phase, for example, a peptide epitope tether which may be bound to a monoclonal antibody attached to an agarose bead.

Specific examples of epitope tethers include, but are not limited to, epitopes
5 for the anti-dynorphin monoclonal antibody 3-E7 (YGGFL(SEQ ID NO:323); Cwiria et al., 1990. Proc. Natl. Acad. Sci. U.S.A. 87:6378-6382; Gramsch et al., 1983, J. Neurochem. 40:1220-1226) and the monoclonal antibody epitope ACLEPYTACD (SEQ ID NO:324).

As another example, as described in Matthews and Wells, 1993,
10 Science 260:1113-1117, a phage display library may express randomized test substrates incorporated between a truncated form of the gene III protein of M13 phage and human growth hormone. Substrate phage may be bound to immobilized human growth hormone binding protein, and then cleaved by incubation with active PSA, thereby releasing phage expressing true PSA
15 substrates.

In preferred, nonlimiting examples of the invention, it may be desirable, when exposing the peptide display clonal library to PSA, to use a relatively low concentration of active PSA, thereby selecting for cleavage of particularly efficient substrates.

20 Following selection of clones expressing test substrates cleaved by PSA, the selected clones may be amplified by propagation in a suitable host organism (such as *Escherichia coli*), and then, preferably, exposure to PSA and selection procedures may be repeated to further enrich for clones expressing true PSA substrates.

25 PSA may be prepared using standard laboratory techniques. However, in a preferred, specific, nonlimiting embodiment of the invention, PSA may be purified from human seminal fluid essentially as described in example section 6, *infra*, wherein the seminal fluid is preferably not lyophilized, but rather diluted in TBS and then purified by anion exchange
30 chromatography. The purity of PSA may be confirmed by silver staining or Coomassie staining of an SDS-polyacrylamide gel; protease activity may be evaluated by zymography on a casein substrate gel.

More preferably, PSA may be prepared using recombinant expression techniques. It has been observed that recombinant PSA was substantially more efficient than naturally occurring PSA in peptide cleavage assays. The nucleotide sequence of PSA cDNA or mRNA is disclosed in
5 GenBank, Acc. No. X05332, Lundwall and Lilja, 1987, FEBS Lett. 214:317-322; and Watt et al., 1986, Proc. Natl. Acad. Sci. U.S.A. 83:3166-3170.

PSA may then be combined with test substrate, preferably at various enzyme/substrate ratios to select, at lower enzyme concentrations, for more efficient substrates. In a nonlimiting example, 250 µg PSA may be
10 combined with 2×10^{10} filamentous phage of a peptide display clonal library in 250 µl TBS, and incubated for about two hours at room temperature or 37°C. Where uncleaved phage harbor an epitope tag, uncleaved phage may then be removed by immunoprecipitation using antibody which binds to the epitope tag. This selection procedure may then be repeated; for example, six
15 successive cycles of the selection procedure may be performed.

Individual clones expressing PSA peptide substrate may then be isolated. The ability of PSA to cleave test substrate expressed by these clones may be tested on an individual basis, for example, using a dot blot analysis as set forth in example section 6, *infra*. Further, the amino acid
20 sequence of the peptide substrate may be determined. Once this sequence has been determined, the corresponding peptide may be synthesized and then tested to confirm that the peptide is actually cleaved by PSA, and with what kinetics. In specific, nonlimiting embodiments of the invention, peptide cleavage may be tested at a 1:10 molar ratio of PSA to peptide, and
25 preferably at a 1:100 molar ratio of PSA to peptide.

5.2. PSA Substrate Compositions

The present invention provides for PSA peptide substrates identified using the methods set forth in the foregoing section. In preferred, nonlimiting embodiments, the kinetics of cleavage of such substrates are
30 such that, for a particular peptide substrate, at least about half of the peptide substrate may be cleaved by PSA in ten minutes at an enzyme to substrate

molar ratio of 1:10. Preferably at least about half of the peptide substrate may be cleaved by PSA in ten minutes at an enzyme to substrate molar ratio of 1:100.

As specific nonlimiting examples, when a peptide display clonal library expressing hexameric test substrates was used to identify PSA substrates, amino acids preferentially occurring at each of the six positions of test substrate hexamers were identified, and are depicted in Figures 1-6. As shown in these figures, at position 1, phenylalanine, leucine, and tyrosine preferentially occurred (Figure 1); at position 2, tyrosine preferentially occurred (Figure 2); at position 3, serine (and to a lesser extent alanine and glycine) preferentially occurred (Figure 3); at position 4, glycine and serine preferentially occurred (Figure 4); at positions 5 and 6, greater variability was observed (Figures 5 and 6).

In further specific, nonlimiting examples, nine consensus peptide sequences have been identified, including LYSGDA (SEQ ID NO:1), LYSGSA (SEQ ID NO:331), LYSGDV (SEQ ID NO:81), LYAGSE (SEQ ID NO:110), LYSGDT (SEQ ID NO:120), YYSGRA (SEQ ID NO:135), YYSGEV (SEQ ID NO:332), KRGRKK (SEQ ID NO:166) and LNSRGN (SEQ ID NO:333). Test substrates corresponding to these sequences which were observed to be cleaved by PSA are set forth in Figures 7-13 and 18. In specific nonlimiting embodiments, the present invention provides for PSA substrates comprising one or more of the foregoing consensus peptide sequences.

In further preferred, specific, nonlimiting embodiments, the present invention provides for PSA substrates comprising a peptide sequence selected from the group consisting of GYYSRDMLV (SEQ ID NO:325), GLYSGTKLV (SEQ ID NO:326), GLYSTESLV (SEQ ID NO:327), GYQSVRMLV (SEQ ID NO:328), and GYYSKNALV (SEQ ID NO:329) see example *infra*). Additional peptides which may be comprised in a PSA substrate according to the invention are set forth in Figure 18.

The foregoing peptide substrates for PSA may be, in nonlimiting embodiments of the invention, comprised in a larger molecule which further

comprises additional peptide or non-peptide components. For example, such peptide substrates may be comprised in a larger peptide or protein and/or may comprise a detectable peptide or non-peptide label moiety. As specific nonlimiting examples, the peptide substrate may be comprised in a larger peptide having 10-100 amino acids, or a protein having 100-200 or 200-500 amino acids. Specific peptide substrates or such substrates comprised in larger molecules are collectively referred to as "PSA substrates".

As a specific, nonlimiting example, a PSA substrate, according to the invention, may comprise a pair of self-quenching fluorophore labels, which when comprised at a distance of about 4-15 amino acids apart, will not appreciably fluoresce, but, if the substrate is cleaved, thereby separating the fluorophores, they may be "dequenched" and emit fluorescent signal(s). See, for example, Proteolytic Enzymes: A Practical Approach, Beynon and Bond, eds., IRL Press at Oxford University Press, New York, esp. pp.38-39.

PSA substrates, according to the invention, may be chemically synthesized or prepared using molecular biological techniques.

5.3. Uses Of PSA Substrates

PSA substrates of the invention may be used in methods to detect and/or measure the amount of enzymatically active PSA. In a first series of nonlimiting embodiments, PSA substrates may be used to identify compounds which inhibit the enzymatic activity of PSA. The favorable cleavage kinetics of such substrates may facilitate screening a multitude of compounds. For example, compounds generated by combinatorial chemistry techniques may each be tested for their ability to inhibit the activity of PSA to cleave one or more PSA substrates.

PSA substrates of the invention may also be used as a basis for rational drug design of PSA inhibitors. For example, a PSA substrate peptide may be used as a basis for the synthesis of a non-cleavable analog. Inhibitor design may be facilitated by crystallographic analysis of PSA and the substrate, or of a co-crystal formed between PSA and its substrate. Crystallographic analysis may provide information relating to the interaction

between PSA substrate and the enzyme active site which may be used to design an appropriate inhibitor using structure-based drug design techniques known in the art. Inhibitors prepared using standard medicinal chemistry techniques may be or comprise peptide, or may be peptidomimetic.

5 PSA inhibitors identified according to the invention may be used as chemotherapeutic agents in the treatment or prevention of prostate cancer. For example, such inhibitors may be useful in the treatment of subjects having an elevation of serum PSA without overt malignancy. Such inhibitors may also be useful in the treatment of subjects diagnosed as suffering from
10 prostate carcinoma, but where the efficacy of surgery is disputed. Alternatively, such inhibitors may be used in the treatment of subjects suffering from prostate cancer in conjunction with surgery, radiotherapy, chemotherapy and/or hormonal therapy, wherein the use of two distinct therapeutic pathways would be expected to be more effective than use of a
15 single modality. PSA inhibitors identified according to the invention may prove, in these various contexts, effective in preventing and/or deterring the occurrence, progression, or metastasis of prostate carcinoma. In related embodiments, inhibitors of PSA may be used to block other physiologic functions of PSA.

20 In a further series of nonlimiting embodiments, PSA substrates of the invention may be used to detect and/or measure the amount of active PSA in a sample (e.g., a serum sample or a tissue sample, such as a tumor sample) collected from a patient. The presence of active PSA in the sample may bear a positive correlation with the presence of a malignant, and
25 particularly a metastatic malignant, disease.

 In a related series of nonlimiting embodiments, assays using PSA substrates of the invention, which evaluate the presence and/or level of enzymatically active PSA, may be used to adjust the dose of therapeutic agent(s) in a patient. For example, the level of active PSA in a patient serum
30 sample before and/or after a given dose of therapeutic agent(s) may be determined, and the dose of therapeutic agent may be adjusted until the serum level of active PSA significantly decreases or becomes absent.

For purposes of illustration, and not by way of limitation, the following working example is provided.

6. Example: Identification Of PSA Substrates

6.1. PSA Purification From Seminal Plasma

5 Human ejaculate was collected and frozen by volunteer subjects, and stored at -80°C. Prior to use, the sample was thawed, allowed to liquefy, and then sperm were removed by low speed centrifugation (4000 rpm for 15 minutes using a Sorvall SS-34 rotor at room temperature). The resulting seminal fluid supernatant was further clarified by high speed
10 centrifugation (20,000 rpm for 20 minutes using a Sorvall SS-34 rotor at 4°C). The clarified seminal fluid (50ml) was precipitated with 50% ammonium sulfate and centrifuged (10,000 rpm for 30 minutes using a Sorvall SS-34 rotor at 4°C). The resulting pellet was then resuspended in 1/10 the original volume in Buffer A (phosphate 10 mM, pH 6.9), and dialyzed against 100
15 volumes of the same buffer. The dialyzed solution was clarified by centrifugation (10,000 rpm for 15 minutes using a Sorvall S-34 rotor at 4°C) and then filtered through a 0.22 µm Millipore filter.

The sample was then applied at a flow rate of 3 ml/min to a SP Sepharose HP FPLC column (XK 26/60; Pharmacia LKB) equilibrated with
20 Buffer A. The column was washed with 10 bed volumes, and the bound proteins were subsequently eluted with a linear gradient of Buffer B (phosphate 10 mM, pH 6.9, NaCl 500 mM) at a flow rate of 3 ml/min for 180 minutes. Fractions were collected. PSA purification was monitored by silver staining of SDS-polyacrylamide (10%) resolving gels of the column fractions,
25 and by separately performing western blot analysis using polyclonal antibody directed against human PSA (Dakko). PSA activity was monitored by casein substrate zymography (0.25-1 mg/ml) in a 10% resolving gel. Fractions containing PSA activity and immunoreactivity were immediately pooled and dialyzed against Buffer A. The dialyzed sample was then filtered and applied
30 to a Source S (Pharmacia LKB) column equilibrated with Buffer A. The column was washed and bound proteins were eluted with a linear gradient of

Buffer B in 60 minutes. The fractions were analyzed by silver staining/western blot/zymography as set forth above. PSA-containing fractions were then reappplied to the same column for a second round of purification under identical conditions. Figure 14 depicts silver staining/western blot/zymography analysis of FPLC fractions of the final PSA purification steps.

6.2. Preparation of Recombinant PSA

Cos-7 cells were transfected with a cDNA coding for human PSA cloned into a pCDNA3 expression vector (Invitrogen). Transfection was performed by electroporation with a BioRad mammalian gene pulser at 200 mV, 500 μ F (high capacity) using 0.25 μ g DNA per cm^2 cell surface. $2-3 \times 10^6$ cells were grown in a 15 cm tissue culture plate in DME medium containing 5% fetal calf serum. The conditioned medium was collected after 2 days and 3 days, yielding a total of 350 mls. The medium was precipitated by 50% ammonium sulfate and centrifuged at 10,000 rpm for 20 minutes in a Sorvall GSA rotor. The resulting pellet was reconstituted in 1/10 the original volume in Buffer A, dialyzed against Buffer A, and filtered as described above. The sample was then applied to a Sp Sepharose HP (XK 16/20) column at 1 ml/min. The column was washed several times and then eluted with a linear gradient of Buffer B at 1ml/min. in 30 minutes. The purification was monitored using a silver staining and western blot analysis, as described above.

6.3. Identification Of PSA Peptide Substrates

Library screening and phage selection. 2×10^6 phage (20 μ l of the ftc-LIB-N6 library; Affymax) were digested with 250 μ g of purified PSA (as determined using BCA protein assay) in TBS in a total volume of 250 μ l for 2 hours at 37°C. A control reaction was performed under the same conditions, but without PSA. The reaction was then stopped by the addition of ZnCl_2 to 1 mM. 30 μ l of 1% BSA and 10 μ l (100 μ g) of monoclonal antibody 3-E7 (Gramsch Laboratories, Germany) was then added. The reaction

mixture was kept on ice for 30 minutes, after which 100 µl of pansorbin cells (protein A-expressing bacterial ghosts, used to bind antibodies) were added, then rotated for 1 hour at 4°C and centrifuged at 12,000g for 2 minutes in a Sorvall MC 12V centrifuge. The supernatant was recovered, and the
5 pansorbin step repeated. The final supernatant phage preparation was titered on LB/tetracycline (15 µg/ml) plates and amplified overnight.

K91 cell culture. K91 cells were used as phage host bacteria. This bacterial strain does not carry any selection markers for growth in antibiotics or other conditions. K91 cells were grown in LB medium to log
10 phase and used for titration of phage. A 10-fold concentrated bacterial stock was also made by centrifuging an aliquot (20 ml) of the log phase culture at 12,000g for 10 minutes in a Sorvall MC 12V centrifuge and resuspending the bacterial pellet in 2 ml of TBS. The 10-fold bacterial stock was used for transformation of amplified phage in each round of screening. A fresh batch
15 of bacteria and 10-fold stock was made every day as needed and stored at 4°C.

Phage titration. A small aliquot of phage supernatant was diluted 10^{-3} to 10^{-7} times in TBS. 10 µl of each phage dilution was mixed with 100 µl of K91 bacteria for 20 minutes at 37°C and plated on LB/tetracycline
20 (15 µg/ml) plates overnight at 37°C. The phage contain a tetracycline resistance gene, so that infected bacteria survive under selection conditions. The next day, clones present on each dish were counted.

Phage amplification. The remainder of immunodepleted phage supernatant was mixed with 10-fold concentrated K91 bacteria, incubated for
25 20 minutes at 37°C, added to 100 ml of LB/tetracycline (15 µg/ml) and grown with shaking overnight at 37°C. The bacteria were removed by centrifugation at 12,000g (GSA rotor, Sorvall) for 15 minutes. The phage present in the supernatant were precipitated by addition of polyethyleneglycol (PEG, 20 ml of 20% PEG, 2.5 M NaCl to 100 ml of phage), precipitated on ice overnight,
30 centrifuged at 12,000g for 15 minutes and drained for 10 minutes. The resulting phage pellet was resuspended in 1 ml of TBS. Any remaining bacteria were removed by centrifugation for 12,000g (Sorvall microfuge) for

10 minutes and incubating the supernatant at 70°C for 10 minutes. This final supernatant was titered as above and used for the next round of screening. For each series, seven rounds of screening were performed.

5 Phage proteolysis assay using dot-blot. 12-24 clones resulting
from each round of screening were randomly selected from the titer plates
and grown in 2 ml of LB/tetracycline (15 µg/ml). The phage were precipitated
as above. The phage pellet was resuspended in 10 µl of TBS, transferred to
96-well plates and kept on ice. 90 µl of PSA in TBS was added to each well
to a final PSA concentration of 50 µg/ml, and incubated at 37°C. At various
10 time points, 30 µl samples were removed and added to 70 µl of TBS/1 mM
ZnCl₂. The samples were spotted onto a nitrocellulose filter using a vacuum
dot-blotter (Schleicher & Schuell). The filter was blocked by incubation in 5%
non-fat milk in TBS-T (TBS, 0.05% Tween-20) for 30 minutes, washed three
times, 10 minutes each, with TBS-T, and then incubated for 1 hour with mAb
15 3-E7 at 1 µg/ml in TBS-T. The wash was repeated and the filter incubated
with secondary antibody (goat anti-mouse IgG horse radish peroxidase
conjugate; BioRad) at 1:5000 dilution in TBS-T for 1 hour. The filter was
washed as before, and the presence on antibodies was visualized using
chemiluminescence detection (ECL kit, Amersham) to expose Kodak X-AR
20 film, which was subsequently developed. Based on the rate of removal of
signal, the effectiveness of PSA substrate, expressed in the context of phage
protein, was scored from (-) negative to (++++), to indicate highly efficient
substrate (see Figure 15). Figure 18 lists various peptides which were
determined to be cleaved by PSA using dot blot analysis.

25 Peptide synthesis. Synthetic peptide substrates were
synthesized by the Memorial Sloan-Kettering microchemistry facility using an
ABI 433 peptide synthesis apparatus in combination with Fmoc chemistry,
and prepared with a blocked acetylated amino terminus.

30 Peptide site of cleavage by PSA. The site of hydrolysis of the
peptides was determined by matrix assisted laser desorption ionization time
of flight mass spectrometry (PerSeptive BioSystems Voyager RP). This
technique allows an accurate determination of the molecular weight of

cleavage products resulting from treatment with PSA, and the molecular weight can be used to determine the exact position of cleavage.

Kinetic analysis of peptides. Hydrolysis of peptides was determined using a fluorescamine assay. Various concentrations of peptides
5 were incubated with an empirically determined amount of PSA at 37°C in assay buffer (Tricine 50 mM, pH 7.5, NaCl 200 mM, CaCl₂ 10 mM) for various times. Cleavage of peptide was then measured using a Perkin Elmer Fluorimeter at an excitation wavelength of about 394 nanometers, and an emission wavelength of about 494 nanometers.

10 Figure 16 depicts cleavage of various peptides by naturally occurring PSA, at a 1:100 molar PSA/peptide ratio. As illustrated by Figure 17, recombinant PSA was found to be much more efficient at cleaving peptide MR2 (GYYSRDMLV; SEQ ID NO:330). Accordingly, recombinant PSA may be used to identify substrates at even lower PSA/peptide ratios; such
15 substrates may prove to be especially efficient in assays to identify PSA inhibitors.

Various publications are cited herein, the contents of which are hereby incorporated, by reference, in their entireties.

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Sloan Kettering Institute ... and Rothman et al.

5 (ii) TITLE OF THE INVENTION: Prostate Specific Antigen
Substrates

(iii) NUMBER OF SEQUENCES: 333

(iv) CORRESPONDENCE ADDRESS:

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(B) STREET: 30 Rockefeller Plaza
(C) CITY: New York
(D) STATE: NY
(E) COUNTRY: U.S.A.
(F) ZIP: 10112-0228

(v) COMPUTER READABLE FORM:

15 (A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ Version 2.0

(vi) CURRENT APPLICATION DATA:

20 (A) APPLICATION NUMBER:
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(vii) PRIOR APPLICATION DATA:

25 (A) APPLICATION NUMBER: 60/040,174
(B) FILING DATE: 11 March 1997

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Kole, Lisa B.
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(C) REFERENCE/DOCKET NUMBER:

30 (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 212-705-5000
(B) TELEFAX: 212-705-5020
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Leu Tyr Ser Gly Asp Ala
1 5

10 (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Leu Tyr Glu Gly Gly Thr
1 5

20 (2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Phe Tyr Ser Asp Arg Glu
1 5

30 (2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

5 Ser Tyr Thr Gly Asn Met
 1 5

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

15 Arg Tyr Ser Gly Asn Gly
 1 5

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

20

(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

25 Leu Tyr Lys Gly Asn Leu
 1 5

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Phe Tyr Arg Ser Asp Lys
1 5

5 (2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

10 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ser Tyr Ala Ser Thr Ser
1 5

15 (2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

20 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Leu Tyr Ser Thr Glu Ser
1 5

25 (2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

30 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

21

Arg Tyr Glu Met Asp Val
1 5

(2) INFORMATION FOR SEQ ID NO:11:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

- 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Val Tyr Ala Ser Arg Gly
1 5

(2) INFORMATION FOR SEQ ID NO:12:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

- 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Phe Tyr Val Ser Met Phe
1 5

(2) INFORMATION FOR SEQ ID NO:13:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

- 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Leu Tyr Ser Ser Asp Leu
1 5

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

10 Tyr Tyr Ser Asp Ser Val
1 5

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

20 Ile Tyr Ser Met Gly Asn
1 5

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

30 Tyr Gln Ser Thr Pro Asp
1 5

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

23

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Leu Tyr Ser Ser Ser Val
1 5

(2) INFORMATION FOR SEQ ID NO:18:

- 10 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Val Tyr Ser Ser Asp Asn
1 5

(2) INFORMATION FOR SEQ ID NO:19:

- 20 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Tyr Gln Ser Val Arg Met
1 5

(2) INFORMATION FOR SEQ ID NO:20:

- 30 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 6 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

5 His Tyr Gly Phe Lys Pro
 1 5

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

15 Leu Tyr Glu Gly Ser Glu
 1 5

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

25 Tyr Ile Ser Val Pro Gly
 1 5

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Tyr Tyr Arg Ser Arg Gln
1 5

(2) INFORMATION FOR SEQ ID NO:24:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 10 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Tyr Thr Ala Gly Ser Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:25:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 20 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Leu Tyr Ser Gly Lys Gly
1 5

(2) INFORMATION FOR SEQ ID NO:26:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 30 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Leu Tyr Arg Gly Asp Asp

1

5

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

10

Ile Tyr Ser Ser Ser Ser
1 5

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Leu Tyr Thr Asp Gly Phe
1 5

(2) INFORMATION FOR SEQ ID NO:29:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 10 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Gln Tyr Thr Gly Ser Thr
1 5

(2) INFORMATION FOR SEQ ID NO:30:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 20 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Tyr Tyr Gln Val Ser Asn
1 5

(2) INFORMATION FOR SEQ ID NO:31:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 30 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Tyr Tyr Gln Gln Gly Asp
1 5

(2) INFORMATION FOR SEQ ID NO:32:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Tyr Thr Asn Ser Asp Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:33:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Ile Tyr Glu Gly Arg Ala
1 5

(2) INFORMATION FOR SEQ ID NO:34:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Thr Tyr Met Gly Ser Ser
1 5

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

10 Met Tyr Gln Gly Arg His
1 5

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

20 Phe Tyr His Arg His Arg
1 5

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Ser Tyr Ser Gly Asp Leu
1 5

(2) INFORMATION FOR SEQ ID NO:38:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Gln Tyr Ala Ser Asp Ser
1 5

(2) INFORMATION FOR SEQ ID NO:39:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Ala Tyr Arg Gly Glu Gln
1 5

(2) INFORMATION FOR SEQ ID NO:40:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Lys Tyr Ala Ala Asp Val

1

5

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

10

Phe Tyr Thr Ala Asp Ser

1

5

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

20

Tyr Tyr Ser Lys Asn Ala

1

5

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Ser Tyr Ser Ala Asp Ala
1 5

(2) INFORMATION FOR SEQ ID NO:44:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Tyr Tyr Glu Gly Ser Met
1 5

(2) INFORMATION FOR SEQ ID NO:45:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Ser Tyr Ser Gly Gly Asn
1 5

(2) INFORMATION FOR SEQ ID NO:46:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Met Tyr Ser Ala Asp Ala

1

5

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

10

Phe Tyr Val Ser Glu Ala

1

5

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

20

Leu Tyr His Ser Asp Asn

1

5

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Tyr Tyr Ser Arg Pro Val
1 5

(2) INFORMATION FOR SEQ ID NO:50:

5 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Leu Tyr Thr His Gln Val
1 5

(2) INFORMATION FOR SEQ ID NO:51:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Tyr Tyr Ser Arg Asp Met
1 5

(2) INFORMATION FOR SEQ ID NO:52:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Phe Tyr His Gly Asn Arg

1

5

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

10

Tyr Tyr Ser Asp Arg Lys
1 5

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

20

His Thr Glu Gly Gly Met
1 5

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Val Tyr Ser Asn Asp Lys
1 5

(2) INFORMATION FOR SEQ ID NO:56:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 10 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Met Tyr Asn Gly Leu Gly
1 5

(2) INFORMATION FOR SEQ ID NO:57:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 20 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Tyr Tyr Ala Asp Arg Ala
1 5

(2) INFORMATION FOR SEQ ID NO:58:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 30 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Val Tyr Thr Gly Gly Ala

1

5

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

10

Leu Tyr Ser Ser Ser Thr

1

5

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

20

Phe Tyr Arg Ser Asn Thr

1

5

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Val Tyr His Gly Ser Ala
1 5

(2) INFORMATION FOR SEQ ID NO:62:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 10 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Phe Tyr Asp Ser Asn Val
1 5

(2) INFORMATION FOR SEQ ID NO:63:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 20 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Phe Tyr Ser Gly Glu Glu
1 5

(2) INFORMATION FOR SEQ ID NO:64:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 30 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Tyr Gln Ala Ser Ser Tyr

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(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

5

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

10

Asn Tyr Ser Gly Arg Lys

1

5

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

20

His Tyr Ala Ala Asn Asn

1

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(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 6 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Asn Tyr Ala Gly Ser Gly
1 5

(2) INFORMATION FOR SEQ ID NO:68:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Asn Tyr Thr Arg Glu Phe
1 5

(2) INFORMATION FOR SEQ ID NO:69:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Asn Tyr Asp Gly Gly Val
1 5

(2) INFORMATION FOR SEQ ID NO:70:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Leu Tyr Arg Gly Lys Glu

1

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(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

10

Val Tyr Lys Gly Gly Glu
1 5

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

20

Leu Tyr Pro Trp Phe Ser
1 5

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Leu Tyr Asn Asn Glu Ala
1 5

(2) INFORMATION FOR SEQ ID NO:74:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Asn Tyr Ser Val Glu Val
1 5

(2) INFORMATION FOR SEQ ID NO:75:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Tyr Met Ala Gly Ser Thr
1 5

(2) INFORMATION FOR SEQ ID NO:76:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Phe Tyr Ala Glu His Thr

1

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(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

10

His Tyr Gly Met Asp Val
1 5

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

20

Pro Tyr Gln Gly Gly Glu
1 5

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Leu Tyr Gln Gly Glu Asp
1 5

(2) INFORMATION FOR SEQ ID NO:80:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Arg Tyr Glu Gly Asn Ala
1 5

(2) INFORMATION FOR SEQ ID NO:81:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Leu Tyr Ser Gly Asp Val
1 5

(2) INFORMATION FOR SEQ ID NO:82:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Leu Tyr Glu Gly Gly Thr

45

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(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

10

Arg Tyr Ser Gly Asn Gly
1 5

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

20

Leu Tyr Ser Ser Asp Leu
1 5

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Tyr Tyr Ser Asp Ser Val
1 5

(2) INFORMATION FOR SEQ ID NO:86:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Leu Tyr Ser Ser Ser Val
1 5

(2) INFORMATION FOR SEQ ID NO:87:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Val Tyr Ser Ser Asp Asn
1 5

(2) INFORMATION FOR SEQ ID NO:88:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Leu Tyr Ser Gly Thr Lys

1

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(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

10

Phe Tyr His Arg His Arg
1 5

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

20

Ser Tyr Ser Gly Asp Leu
1 5

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Leu Tyr Ser Gly Lys Gly
1 5

(2) INFORMATION FOR SEQ ID NO:92:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

Phe Tyr Thr Ala Asp Ser
1 5

(2) INFORMATION FOR SEQ ID NO:93:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Tyr Tyr Ser Arg Asp Met
1 5

(2) INFORMATION FOR SEQ ID NO:94:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

His Tyr Glu Gly Gly Met

1

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(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

10

Val Tyr Thr Gly Gly Ala
1 5

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

20

Tyr Tyr Glu Gly Ser Met
1 5

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Ser Tyr Ser Gly Gly Asn
1 5

(2) INFORMATION FOR SEQ ID NO:98:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Met Tyr Ser Ala Asp Ala
1 5

(2) INFORMATION FOR SEQ ID NO:99:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

Asn Tyr Asp Gly Gly Val
1 5

(2) INFORMATION FOR SEQ ID NO:100:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Val Tyr Lys Gly Gly Glu

1

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(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

10

Phe Tyr Asp Ser Asn Val

1

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(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

20

Arg Tyr Glu Gly Asn Ala

1

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(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

Phe Tyr Ser Gly Glu Glu
1 5

(2) INFORMATION FOR SEQ ID NO:104:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

Tyr Ala Ser Ser Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:105:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

Asn Tyr Ser Gly Arg Lys
1 5

(2) INFORMATION FOR SEQ ID NO:106:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

Phe Tyr Ala Gln Ser Gln

1

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(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

10

His Tyr Ala Ala Asn Asn
1 5

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

20

Asn Tyr Ala Gly Ser Gly
1 5

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Asn Tyr Thr Arg Glu Phe
1 5

(2) INFORMATION FOR SEQ ID NO:110:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

Leu Tyr Ala Gly Ser Glu
1 5

(2) INFORMATION FOR SEQ ID NO:111:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Phe Tyr Ser Asp Arg Glu
1 5

(2) INFORMATION FOR SEQ ID NO:112:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Ser Tyr Ala Ser Thr Ser

55

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(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

10

Tyr Ile Ser Val Pro Gly
1 5

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

20

Tyr Thr Ala Gly Ser Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Leu Tyr His Ser Asp Asn
1 5

(2) INFORMATION FOR SEQ ID NO:116:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

Leu Tyr Pro Trp Phe Ser
1 5

(2) INFORMATION FOR SEQ ID NO:117:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Tyr Met Ala Gly Ser Thr
1 5

(2) INFORMATION FOR SEQ ID NO:118:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

Pro Tyr Gln Gly Gly Glu Leu

1

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(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

10

Leu Tyr Gln Gly Glu Asp

1

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(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

20

Leu Tyr Ser Gly Asp Thr

1

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(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Leu Tyr Lys Gly Asn Leu
1 5

(2) INFORMATION FOR SEQ ID NO:122:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 10 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Phe Tyr Arg Ser Asp Lys
1 5

(2) INFORMATION FOR SEQ ID NO:123:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 20 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Ile Tyr Ser Met Gly Asn
1 5

(2) INFORMATION FOR SEQ ID NO:124:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 30 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Tyr Gln Ser Thr Pro Asp

1

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(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

10

His Tyr Gly Phe Lys Pro

1

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(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

20

Thr Tyr Met Gly Ser Ser

1

5

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Gln Tyr Ala Ser Asp Ser
1 5

(2) INFORMATION FOR SEQ ID NO:128:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Lys Tyr Ala Ala Asp Val
1 5

(2) INFORMATION FOR SEQ ID NO:129:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Gln Tyr Thr Gly Ser Thr
1 5

(2) INFORMATION FOR SEQ ID NO:130:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Ser Tyr Ser Ala Asp Ala

1

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(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

10

Leu Tyr Ser Ser Ser Thr
1 5

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

20

Phe Tyr Arg Ser Asn Thr
1 5

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

Val Tyr His Gly Ser Ala
1 5

(2) INFORMATION FOR SEQ ID NO:134:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Leu Tyr Arg Gly Lys Glu
1 5

(2) INFORMATION FOR SEQ ID NO:135:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Tyr Tyr Ser Gly Arg Ala
1 5

(2) INFORMATION FOR SEQ ID NO:136:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Ser Tyr Thr Gly Asn Met

1

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(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

10

Arg Leu Ser Met Tyr Gln
1 5

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

20

Phe Tyr Val Ser Met Phe
1 5

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

Tyr Gln Ser Val Arg Met
1 5

(2) INFORMATION FOR SEQ ID NO:140:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 10 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

Ser Tyr Ala Ala Ala Ser
1 5

(2) INFORMATION FOR SEQ ID NO:141:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 20 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

Arg Thr Val Asn Tyr Gly
1 5

(2) INFORMATION FOR SEQ ID NO:142:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 30 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Leu Tyr Glu Gly Ser Glu

65

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(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

10

Tyr Tyr Arg Ser Arg Gln
1 5

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

20

Leu Tyr Ser Thr Glu Ser
1 5

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

Val Tyr Ala Ser Arg Gly
1 5

(2) INFORMATION FOR SEQ ID NO:146:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 10 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

Tyr Thr Asn Ser Asp Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:147:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 20 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

Ile Tyr Glu Gly Arg Ala
1 5

(2) INFORMATION FOR SEQ ID NO:148:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 30 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

Met Tyr Gln Gly Arg His

1

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(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

10

Ala Tyr Arg Gly Glu Gln

1

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(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

20

Ile Tyr Ser Ser Ser Ser

1

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(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

Leu Tyr Thr Asp Gly Phe
1 5

(2) INFORMATION FOR SEQ ID NO:152:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

Ala Tyr Ala Gly Gly Gly
1 5

(2) INFORMATION FOR SEQ ID NO:153:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Tyr Tyr Gln Val Ser Asn
1 5

(2) INFORMATION FOR SEQ ID NO:154:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

Tyr Tyr Gln Gln Gly Asp

1

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(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

10

Tyr Tyr Ser Lys Asn Ala
1 5

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

20

Phe Tyr His Gly Asn Arg
1 5

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

Met Tyr Asn Gly Leu Gly
1 5

(2) INFORMATION FOR SEQ ID NO:158:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

Tyr Tyr Ala Asp Arg Ala
1 5

(2) INFORMATION FOR SEQ ID NO:159:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

Phe Tyr Val Ser Glu Ala
1 5

(2) INFORMATION FOR SEQ ID NO:160:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

Tyr Tyr Ser Arg Pro Val

71

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(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

10

Leu Tyr Thr His Gln Val
1 5

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

20

Tyr Gln Ser Ser Gly Ser
1 5

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

Leu Tyr Asn Asn Glu Ala
1 5

(2) INFORMATION FOR SEQ ID NO:164:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

Asn Tyr Ser Val Glu Val
1 5

(2) INFORMATION FOR SEQ ID NO:165:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

Phe Tyr Ala Asp His Thr
1 5

(2) INFORMATION FOR SEQ ID NO:166:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

Lys Arg Gly Arg Lys Lys

1

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(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

10

Lys Arg Trp Arg Ser Gly
1 5

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

20

Ser Leu Arg Ser Lys Lys
1 5

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

Asn Val Lys Gln Gly Val
1 5

(2) INFORMATION FOR SEQ ID NO:170:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 10 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

Lys Glu Arg Leu Pro Glu
1 5

(2) INFORMATION FOR SEQ ID NO:171:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 20 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

Asp Asn Met Asn Ser Arg
1 5

(2) INFORMATION FOR SEQ ID NO:172:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 30 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Lys Lys Gly Arg Ala Val

75

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(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

10

Gln Asp Thr Val Lys Asn

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(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

20

Ser Arg Ser Asn Arg Lys

1

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(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

Lys Met Leu Arg Lys Ala
1 5

(2) INFORMATION FOR SEQ ID NO:176:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 10 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Ala Ser Thr His Gly Lys
1 5

(2) INFORMATION FOR SEQ ID NO:177:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 20 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

Met Tyr Gly Arg Thr Asn
1 5

(2) INFORMATION FOR SEQ ID NO:178:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 30 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

Leu Asn Ser Arg Gly Asn

1

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(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

10

Leu Arg Trp Arg Ser Gly
1 5

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

20

Ser Leu Arg Ser Lys Lys
1 5

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

Asn Val Lys Gln Gly Val
1 5

(2) INFORMATION FOR SEQ ID NO:182:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 10 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

Lys Glu Arg Leu Pro Glu
1 5

(2) INFORMATION FOR SEQ ID NO:183:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 20 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

Asp Asn Met Asn Ser Arg
1 5

- 25 (2) INFORMATION FOR SEQ ID NO:184:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
30 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

Lys Lys Gly Arg Ala Val

1

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(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

10

Gln Asp Thr Val Lys Asn
1 5

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

20

Ser Arg Ser Asn Arg Lys
1 5

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

Lys Met Leu Arg Lys Ala
1 5

(2) INFORMATION FOR SEQ ID NO:188:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

Ala Ser Thr His Gly Lys
1 5

(2) INFORMATION FOR SEQ ID NO:189:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

Arg Asp Asp Val Gly Asn
1 5

(2) INFORMATION FOR SEQ ID NO:190:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

Ser Asn Asn Met Asn Glu

1

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(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

10

Trp Ser Cys Cys Asp Ser
1 5

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

20

Lys Asn Lys Ser Arg Val
1 5

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

Leu Phe Ser Gly Asn Glu
1 5

(2) INFORMATION FOR SEQ ID NO:194:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

Phe Asn Ser Ala Asp Trp
1 5

(2) INFORMATION FOR SEQ ID NO:195:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

Arg Ser Ala Gly Leu Asn
1 5

(2) INFORMATION FOR SEQ ID NO:196:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

Leu Asp Asp Ile Pro Ala

1

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(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

10

Leu Thr Leu Glu Thr Asn

1

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(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

20

Leu Tyr Ser Gly Ser Ala

1

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(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

Tyr Tyr Gln Gln Gly Asp
1 5

(2) INFORMATION FOR SEQ ID NO:200:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

Tyr Tyr Ser Lys Asn Ala
1 5

(2) INFORMATION FOR SEQ ID NO:201:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

Tyr Tyr Ser Arg Asp Met
1 5

(2) INFORMATION FOR SEQ ID NO:202:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

Phe Tyr His Gly Asn Arg

1

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(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

10

Tyr Tyr Ser Asp Arg Lys
1 5

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

20

His Tyr Glu Gly Gly Met
1 5

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

Val Tyr Ser Asn Asp Lys
1 5

(2) INFORMATION FOR SEQ ID NO:206:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 10 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

Met Tyr Asn Gly Leu Gly
1 5

(2) INFORMATION FOR SEQ ID NO:207:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 20 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

Tyr Tyr Ala Asp Arg Ala
1 5

(2) INFORMATION FOR SEQ ID NO:208:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 30 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

Val Tyr Thr Gly Gly Ala

1

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(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

10

Ser Tyr Ser Ala Asp Ala
1 5

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

20

Leu Tyr Ser Ser Ser Thr
1 5

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

Phe Tyr Arg Ser Asn Thr
1 5

(2) INFORMATION FOR SEQ ID NO:212:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

Val Tyr His Gly Ser Ala
1 5

(2) INFORMATION FOR SEQ ID NO:213:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

Tyr Tyr Glu Gly Ser Met
1 5

(2) INFORMATION FOR SEQ ID NO:214:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

Ser Tyr Ser Gly Gly Asn

1

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(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

10

Met Tyr Ser Ala Asp Ala

1

5

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

20

Phe Tyr Val Ser Glu Ala

1

5

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

Leu Tyr His Ser Asp Asn
1 5

(2) INFORMATION FOR SEQ ID NO:218:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

Tyr Tyr Ser Arg Pro Val
1 5

(2) INFORMATION FOR SEQ ID NO:219:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

Leu Tyr Thr His Gln Val
1 5

(2) INFORMATION FOR SEQ ID NO:220:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

Tyr Gln Ser Ser Gly Ser

1

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(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

10

Asn Tyr Asp Gly Gly Val
1 5

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

20

Leu Tyr Arg Gly Lys Glu
1 5

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

Val Tyr Lys Gly Gly Glu
1 5

(2) INFORMATION FOR SEQ ID NO:224:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

Leu Tyr Pro Trp Phe Ser
1 5

(2) INFORMATION FOR SEQ ID NO:225:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

Leu Tyr Asn Asn Glu Ala
1 5

(2) INFORMATION FOR SEQ ID NO:226:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

Asn Tyr Ser Val Glu Val

1

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(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

10 Tyr Met Ala Gly Ser Thr
1 5

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

20 Phe Tyr Ala Asp His Thr
1 5

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

His Tyr Gly Met Asp Val
1 5

(2) INFORMATION FOR SEQ ID NO:230:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

Phe Tyr Asp Ser Asn Val
1 5

(2) INFORMATION FOR SEQ ID NO:231:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

Pro Tyr Gln Gly Gly Glu Leu
1 5

(2) INFORMATION FOR SEQ ID NO:232:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

Leu Tyr Gln Gly Glu Asp

1

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(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

10

Arg Tyr Glu Gly Asn Ala
1 5

(2) INFORMATION FOR SEQ ID NO:234:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

20

Phe Tyr Ser Gly Glu Glu
1 5

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

Tyr Gln Ala Ser Ser Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:236:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

Asn Tyr Ser Gly Arg Lys
1 5

(2) INFORMATION FOR SEQ ID NO:237:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

Phe Tyr Ala Gln Ser Gln
1 5

(2) INFORMATION FOR SEQ ID NO:238:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

His Tyr Ala Ala Asn Asn

1

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(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

10

Asn Tyr Ala Gly Ser Gly

1

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(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

20

Asn Tyr Thr Arg Glu Phe

1

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(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

Leu Tyr Glu Gly Gly Thr
1 5

(2) INFORMATION FOR SEQ ID NO:242:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

Arg Tyr Ser Gly Asn Gly
1 5

(2) INFORMATION FOR SEQ ID NO:243:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

Leu Tyr Lys Gly Asn Leu
1 5

(2) INFORMATION FOR SEQ ID NO:244:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

Phe Tyr Arg Ser Asp Lys

1

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(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

10

Phe Tyr Ser Asp Arg Glu

1

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(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

20

Ser Tyr Thr Gly Asn Met

1

5

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

Phe Val Ser Met Phe
1 5

(2) INFORMATION FOR SEQ ID NO:248:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 10 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

Leu Tyr Ser Ser Asp Leu
1 5

(2) INFORMATION FOR SEQ ID NO:249:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 20 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

Tyr Tyr Ser Asp Ser Val
1 5

(2) INFORMATION FOR SEQ ID NO:250:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 30 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

Ile Tyr Ser Met Gly Asn

1

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(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

10 Tyr Gln Ser Thr Pro Asp
1 5

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

20 Leu Tyr Ser Ser Ser Val
1 5

(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

Val Tyr Ser Ser Asp Asn
1 5

(2) INFORMATION FOR SEQ ID NO:254:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

Tyr Gln Ser Val Arg Met
1 5

(2) INFORMATION FOR SEQ ID NO:255:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

Ser Tyr Ala Ser Thr Ser
1 5

(2) INFORMATION FOR SEQ ID NO:256:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

His Tyr Gly Phe Lys Pro

1

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(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

10

Leu Tyr Glu Gly Ser Glu
1 5

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

20

Tyr Ile Ser Val Pro Gly
1 5

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

Tyr Tyr Arg Ser Arg Gln
1 5

(2) INFORMATION FOR SEQ ID NO:260:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

Leu Tyr Ser Thr Glu Ser
1 5

(2) INFORMATION FOR SEQ ID NO:261:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

Arg Tyr Glu Met Asp Val
1 5

(2) INFORMATION FOR SEQ ID NO:262:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

Val Tyr Ala Ser Arg Gly

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(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

10

Leu Tyr Ser Gly Thr Lys
1 5

(2) INFORMATION FOR SEQ ID NO:264:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

20

Tyr Thr Ala Gly Ser Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

Tyr Thr Asn Ser Asp Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:266:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 10 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

Ile Tyr Glu Gly Arg Ala
1 5

(2) INFORMATION FOR SEQ ID NO:267:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 20 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

Thr Tyr Met Gly Ser Ser
1 5

(2) INFORMATION FOR SEQ ID NO:268:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 30 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

Met Tyr Gln Gly Arg His

107

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(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

10

Phe Tyr His Arg His Arg
1 5

(2) INFORMATION FOR SEQ ID NO:270:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

20

Ser Tyr Ser Gly Asp Leu
1 5

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

Gln Tyr Ala Ser Asp Ser
1 5

(2) INFORMATION FOR SEQ ID NO:272:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 10 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

Ala Tyr Arg Gly Glu Gln
1 5

(2) INFORMATION FOR SEQ ID NO:273:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 20 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

Leu Tyr Ser Gly Lys Gly
1 5

(2) INFORMATION FOR SEQ ID NO:274:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 30 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

Lys Tyr Ala Ala Asp Val

1

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(2) INFORMATION FOR SEQ ID NO:275:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

10

Phe Tyr Thr Ala Asp Ser

1

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(2) INFORMATION FOR SEQ ID NO:276:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

20

Leu Tyr Arg Gly Asp Asp

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(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

Ile Tyr Ser Ser Ser Ser
1 5

(2) INFORMATION FOR SEQ ID NO:278:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

Leu Tyr Thr Asp Gly Phe
1 5

(2) INFORMATION FOR SEQ ID NO:279:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

Ala Tyr Ala Gly Gly Gly
1 5

(2) INFORMATION FOR SEQ ID NO:280:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

Gln Tyr Thr Gly Ser Thr

111

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(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

10

Tyr Tyr Gln Val Ser Asn
1 5

(2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

20

Tyr Tyr Ser Gly Glu Val
1 5

(2) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

Tyr Met Ser Ser Asp His
1 5

(2) INFORMATION FOR SEQ ID NO:284:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 10 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

Ala Tyr Phe Ala Arg Lys
1 5

(2) INFORMATION FOR SEQ ID NO:285:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 20 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

Leu Tyr Ser Arg Glu Met
1 5

(2) INFORMATION FOR SEQ ID NO:286:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 30 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

Asn Tyr Ala Gly Ser Gly

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(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

10

Tyr Arg Arg Ala Lys Arg
1 5

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

20

Met Tyr Thr Gly Glu Met
1 5

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

Asn Tyr Glu Met Asp Phe
1 5

(2) INFORMATION FOR SEQ ID NO:290:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 10 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

His Tyr Ser Gly Gly Glu
1 5

(2) INFORMATION FOR SEQ ID NO:291:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 20 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

Ser Tyr Ser Ser Glu Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:292:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 30 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

Phe Tyr Glu Gly Asp Asn

115

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(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

10

Tyr Arg Lys Ala Lys Arg
1 5

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

20

Leu Tyr Arg Ser Glu Ala
1 5

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

Tyr Tyr Arg Val Asn Ser
1 5

(2) INFORMATION FOR SEQ ID NO:296:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

Met Tyr Ser Gly Gly Gly
1 5

15 (2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

Asn Tyr Ser Gly Glu Gly
1 5

25 (2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

Phe Tyr Arg Thr Glu Val

1

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(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

10

Phe Tyr Gln Gly Asp Ser
1 5

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

20

Asn Tyr Ser Gly Asp Val
1 5

(2) INFORMATION FOR SEQ ID NO:301:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

Tyr Tyr Lys Ser Glu Asn
1 5

(2) INFORMATION FOR SEQ ID NO:302:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

Thr Tyr Ala Gly Gly Thr
1 5

(2) INFORMATION FOR SEQ ID NO:303:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

Tyr Tyr Ser Val Ser Gln
1 5

(2) INFORMATION FOR SEQ ID NO:304:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

Met Tyr Ser Gly Arg Glu

1

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(2) INFORMATION FOR SEQ ID NO:305:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

10 Tyr Tyr Ala Thr Ser Arg
1 5

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

20 Tyr Tyr Ser Gly Asn Ala
1 5

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

Val Tyr Gly Asn Ser Val
1 5

(2) INFORMATION FOR SEQ ID NO:308:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

Tyr Gln Ala Gly Gly Glu
1 5

(2) INFORMATION FOR SEQ ID NO:309:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

Tyr Tyr Phe Asn Glu Thr
1 5

(2) INFORMATION FOR SEQ ID NO:310:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

Asn Tyr Ser Gly Asp Val

121

1

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(2) INFORMATION FOR SEQ ID NO:311:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

10

Trp Tyr Cys Trp His Ile

1

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(2) INFORMATION FOR SEQ ID NO:312:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

20

His Tyr Ser Gly Gly Glu

1

5

(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

His Tyr Ser Ser Ser Val
1 5

(2) INFORMATION FOR SEQ ID NO:314:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

Gly Tyr Asn Lys Gly Ile
1 5

(2) INFORMATION FOR SEQ ID NO:315:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

Phe Tyr Gln Gly Ser Asp
1 5

(2) INFORMATION FOR SEQ ID NO:316:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

His Tyr Gln Gly Gly Asp

123

1

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(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

10

Tyr Tyr Ala Gly Lys Asp
1 5

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

20

Phe Tyr Gln Gly Ser Asp
1 5

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:

25

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

Phe Tyr Gln Gly Thr Asp
1 5

(2) INFORMATION FOR SEQ ID NO:320:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

Asn Tyr Asp Gly Gly Val
1 5

(2) INFORMATION FOR SEQ ID NO:321:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

Met Tyr Ser Ala Glu Thr
1 5

(2) INFORMATION FOR SEQ ID NO:322:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: None

(ix) FEATURE:

- (D) OTHER INFORMATION: M=A or C, N=A,C,G or T

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

125

CAGMNNMNNM NNMNNMNNMN NACCACTACC ACCGC 35

(2) INFORMATION FOR SEQ ID NO:323:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

Tyr Gly Gly Phe Leu
1 5

(2) INFORMATION FOR SEQ ID NO:324:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

Ala Cys Leu Glu Pro Tyr Thr Ala Cys Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

Gly Tyr Tyr Ser Arg Asp Met Leu Val
1 5

(2) INFORMATION FOR SEQ ID NO:326:

126

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

Gly Leu Tyr Ser Gly Thr Lys Leu Val
1 5

10 (2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

Gly Leu Tyr Ser Thr Glu Ser Leu Val
1 5

20 (2) INFORMATION FOR SEQ ID NO:328:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

Gly Tyr Gln Ser Val Arg Met Leu Val
1 5

(2) INFORMATION FOR SEQ ID NO:329:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 10 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

Gly Tyr Tyr Ser Lys Asn Ala Leu Val
1 5

(2) INFORMATION FOR SEQ ID NO:330:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 20 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

Gly Tyr Tyr Ser Arg Asp Met Leu Val
1 5

(2) INFORMATION FOR SEQ ID NO:331:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- 30 (ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

Leu Tyr Ser Gly Ser Ala

1

5

(2) INFORMATION FOR SEQ ID NO:332:

(i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

10 Tyr Tyr Ser Gly Glu Val
1 5

(2) INFORMATION FOR SEQ ID NO:333:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

20 Leu Asn Ser Arg Gly Asn
1 5

CLAIMS

1. A method of identifying a substrate for prostate specific antigen comprising (i) exposing a peptide display clonal library to active prostate specific antigen; (ii) selecting a clone which displays a peptide that is
5 cleaved by prostate specific antigen; and (iii) identifying and characterizing the cleaved peptide.

2. The method of claim 1, where the molar ratio of prostate specific antigen to peptide in the peptide display clonal library is 1:10.

3. The method of claim 1, where the molar ratio of prostate
10 specific antigen to peptide in the peptide display clonal library is 1:100.

4. The method of claim 1, in which at least about half of the peptide substrate is cleaved by prostate specific antigen in ten minutes.

5. The method of claim 2, in which at least about half of the peptide substrate is cleaved by prostate specific antigen in ten minutes.

15 6. The method of claim 3, in which at least about half of the peptide substrate is cleaved by prostate specific antigen in ten minutes.

7. A substrate for prostate specific antigen comprising a region which is cleaved by prostate specific antigen, wherein the region has a tetrameric amino acid sequence in which the amino acid at the first position is
20 selected from the group consisting of phenylalanine, leucine and tyrosine; the amino acid at the second position is tyrosine; the amino acid at the third position is selected from the group consisting of serine, alanine, and glycine; and the amino acid at the fourth position is selected from the group consisting of glycine and serine.

25 8. A substrate for prostate specific antigen comprising a region which is cleaved by prostate specific antigen, wherein the region has an amino acid sequence selected from the group consisting of LYSGDA (SEQ ID NO:1), LYSGSA (SEQ ID NO:331), LYSGDV (SEQ ID NO:81), LYAGSE (SEQ ID NO:110), LYSGDT (SEQ ID NO:120), YYSGRA (SEQ ID NO:135),
30 YYSGEV (SEQ ID NO:332), KRGRKK (SEQ ID NO:166) and LNSRGN (SEQ ID NO:333).

9. A substrate for prostate specific antigen comprising a region which is cleaved by prostate specific antigen, wherein the region has an amino acid sequence selected from the group consisting of SEQ ID NOS: 2-80.
- 5 10. A substrate for prostate specific antigen comprising a region which is cleaved by prostate specific antigen, wherein the region has an amino acid sequence selected from the group consisting of SEQ ID NOS:82-109.
- 10 11. A substrate for prostate specific antigen comprising a region which is cleaved by prostate specific antigen, wherein the region has an amino acid sequence selected from the group consisting of SEQ ID NOS:111-119.
- 15 12. A substrate for prostate specific antigen comprising a region which is cleaved by prostate specific antigen, wherein the region has an amino acid sequence selected from the group consisting of SEQ ID NOS:121-134.
- 20 13. A substrate for prostate specific antigen comprising a region which is cleaved by prostate specific antigen, wherein the region has an amino acid sequence selected from the group consisting of SEQ ID NOS:136-165.
- 25 14. A substrate for prostate specific antigen comprising a region which is cleaved by prostate specific antigen, wherein the region has an amino acid sequence selected from the group consisting of SEQ ID NOS:167-177.
- 30 15. A substrate for prostate specific antigen comprising a region which is cleaved by prostate specific antigen, wherein the region has an amino acid sequence selected from the group consisting of SEQ ID NOS:179-197.
16. A substrate for prostate specific antigen comprising a region which is cleaved by prostate specific antigen, wherein the region has an amino acid sequence selected from the group consisting of SEQ ID NOS:198-281.

17. A substrate for prostate specific antigen comprising a region which is cleaved by prostate specific antigen, wherein the region has an amino acid sequence selected from the group consisting of SEQ ID NOS:282-321.

5 18. A substrate for prostate specific antigen comprising a region which is cleaved by prostate specific antigen, wherein the region has an amino acid sequence selected from the group consisting of GYYSRDMLV (SEQ ID NO:325), GLYSGTKLV (SEQ ID NO:326), GLYSTESLV (SEQ ID NO:327), GYQSVRMLV (SEQ ID NO:328) and GYYSKNALV (SEQ ID
10 NO:329).

19. A substrate for prostate specific antigen according to any of claims 7-18, further comprising a pair of self-quenching fluorophore labels at a distance of about 4-15 amino acids apart on either side of the site of prostate specific antigen cleavage.

15 20. A method of identifying an inhibitor of prostate specific antigen, comprising determining whether a test compound inhibits the ability of prostate specific antigen to cleave a substrate according to any of claims 7-18, wherein such inhibitory action indicates that the test compound is an inhibitor of prostate specific antigen.

20 21. A method for identifying an inhibitor of prostate specific antigen, comprising determining whether a test compound inhibits the ability of prostate specific antigen to cleave a substrate according to claim 19, wherein such inhibitory action indicates that the test compound is an inhibitor of prostate specific antigen.

25 22. A method of treating or preventing prostate cancer in a subject, comprising administering an effective amount of a prostate specific antigen inhibitor.

23. A method of determining whether metastatic prostate cancer is present in a subject, comprising (i) obtaining a sample from the subject; (ii)
30 determining the amount of enzymatically active prostate specific antigen in the sample, wherein the amount of enzymatically active prostate specific

antigen is determined by measuring the amount of prostate specific antigen substrate according to any of claims 7-18 cleaved by the sample; and (iii) comparing that amount to a control value, wherein an elevated amount of enzymatically active prostate specific antigen relative to the control value has a positive correlation with the presence of metastatic prostate cancer.

24. A method of determining whether metastatic prostate cancer is present in a subject, comprising (i) obtaining a sample from the subject; (ii) determining the amount of enzymatically active prostate specific antigen in the sample, wherein the amount of enzymatically active prostate specific antigen is determined by measuring the amount of prostate specific antigen substrate according to claim 19 cleaved by the sample; and (iii) comparing that amount to a control value, wherein an elevated amount of enzymatically active prostate specific antigen relative to the control value has a positive correlation with the presence of metastatic prostate cancer.

25. The method of claim 23 which is used to design a treatment regimen of a subject suffering from prostate cancer and receiving a therapeutic agent, wherein the dose of therapeutic agent is adjusted to achieve a significant decrease in the level of enzymatically active prostate specific antigen.

26. The method of claim 24 which is used to design a treatment regimen of a subject suffering from prostate cancer and receiving a therapeutic agent, wherein the dose of therapeutic agent is adjusted to achieve a significant decrease in the level of enzymatically active prostate specific antigen.

27. A method of purifying prostate specific antigen from seminal fluid, comprising preparing an unlyophilized sample of seminal fluid, clarifying the sample by high speed centrifugation, precipitating the protein in the sample with ammonium sulfate, and separating prostate specific antigen on an anion exchange chromatography column.

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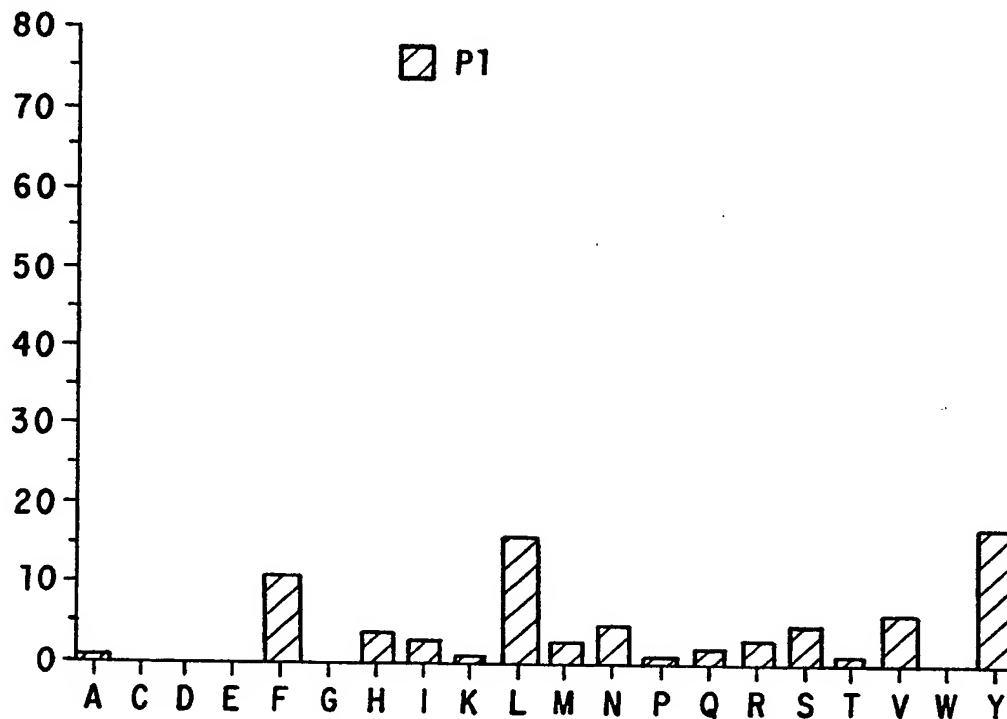


FIG. 1

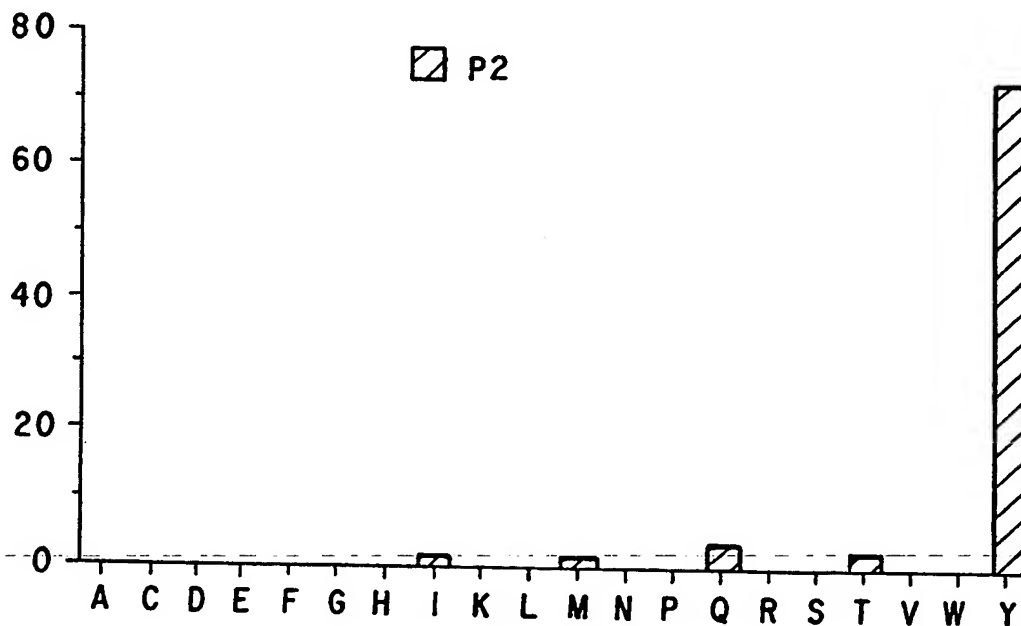


FIG. 2

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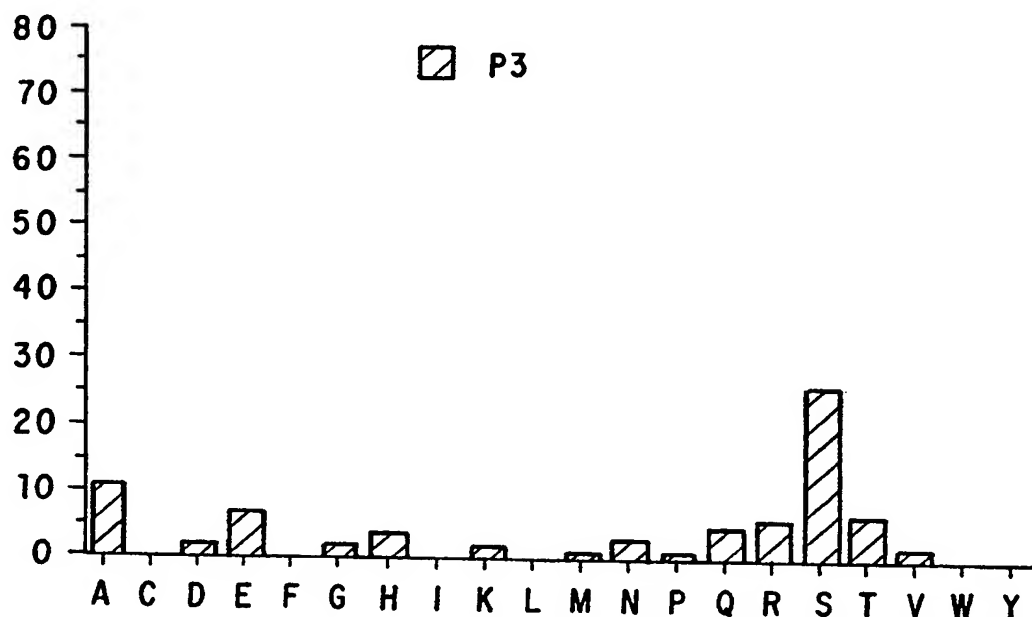


FIG. 3

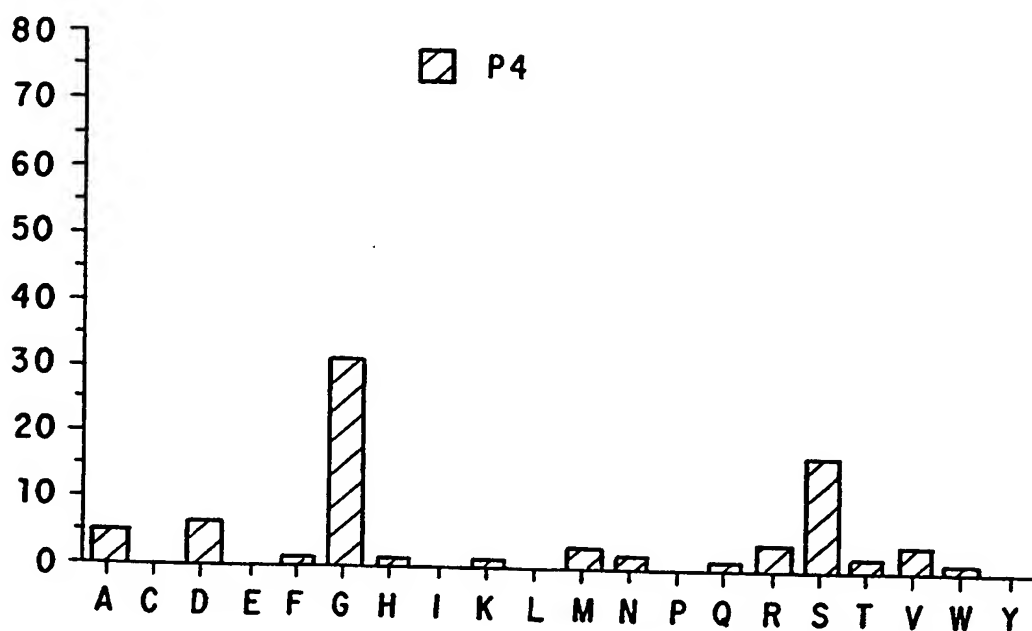


FIG. 4

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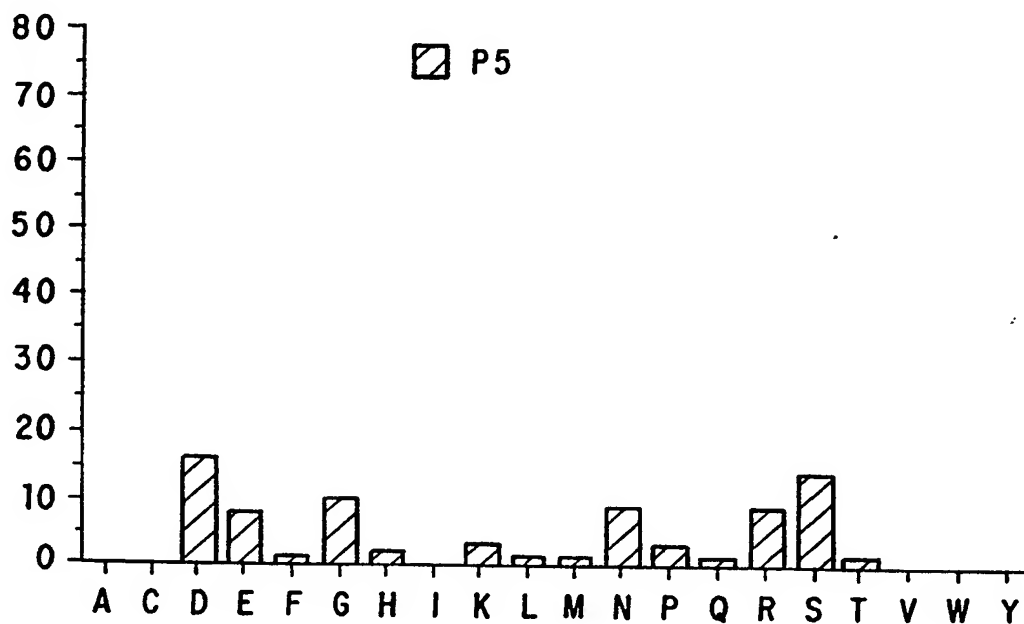


FIG. 5

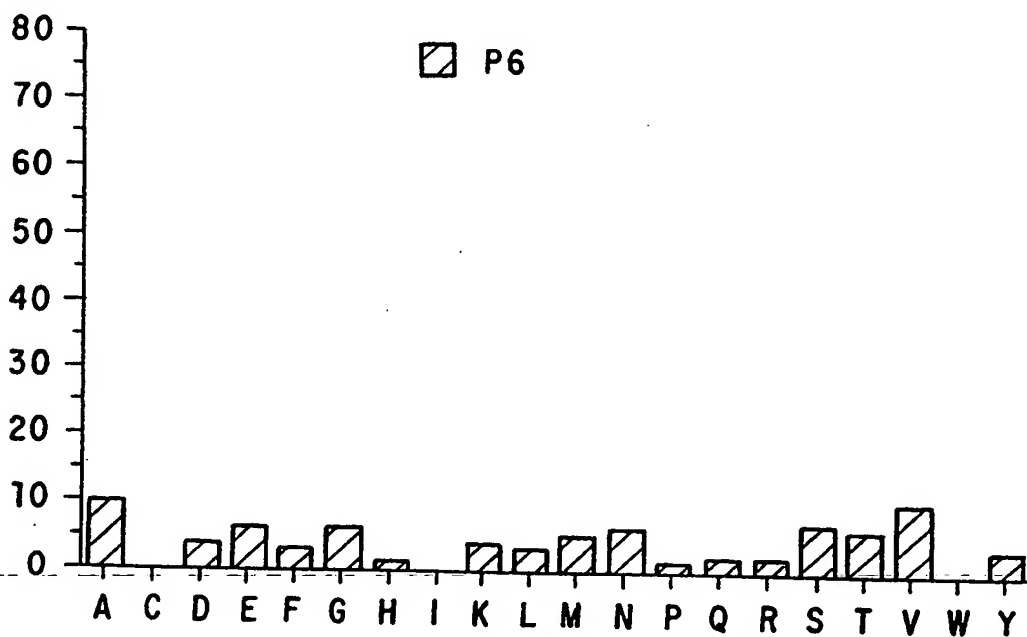


FIG. 6

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LYSGDA-----

10

LYEGGT	SYSADA
FYSDRE	YYEGSM
SYRGNM	SYSGGN
RYSGNG	MYSADA
LYKGNL	FYVSEA
FYRSDK	LYHSDN
SYASTS	YYSRPV
LYSTES	LYTHQV
RYEMDV	YYSRDM
VYASRG	FYHGNR
FYVSMF	YYSDRK
LYSSDL	HYEGGM
YYSDSV	VYSNDK
IYSMGN	MYNGLG
-YQSTPD	YYADRA
LYSSSV	VYTGGA
VYSSDN	LYSSST
-YQSVRM	FYRSNT
HYGFKP	VYHGSA
LYEGSE	FYDSNV
-YISVPG	FYSGEE
YYRSRQ	-YQASSY
-YTAGSY	NYSGRK
LYSGKG	HYAANN
LYRGDD	NYAGSG
IYSSSS	NYTREF
LYTDGF	NYDGGV
QYTGST	LYRGKE
YYQVSN	VYKGGE
YYQQGD	LYPWFS
-YTNSDY	LYNNEA
IYEGRA	NYSVEV
TYMGSS	-YMAGST
MYQGRH	FYADHT
FYHRHR	HYGMDV
SYSGDL	PYQGGE
QYASDS	LYQGED
AYRGEQ	RYEGNA
KYAADV	
EYTADS	
YYSKNA	

FIG.7

SUBSTITUTE SHEET (RULE 26)

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LYSGDV

LYEGGT
RYSNG
LYSSDL
YYSDSV
LYSSSV
VYSSDN
LYSGTK
FYHRHR
SYSGDL
LYSGKG
FYTADS
YYSRDM
HYEGGM
VYTGGA
YYEGSM
SYSGGN
MYSADA
NYDGGV
VYKGGE
FYDSNV
RYEGNA
FYSGEE
YYASSY
NYSGRK
FYAQSO
HYAANN
NYAGSG
NYTREF

FIG.8

LYAGSE-

FYSDRE
SYASTS
YISVPG
YTAGSY
LYHSDN
LYPWFS
YMGST
PYQGGE
LYQGED

FIG.9

LYSGDT

LYKGNL
FYRSDK
IYSMGN
YQSTPD
HYGFKP
TYMGSS
QYASDS
KYAADV
QYTGST
SYSADA
LYSSST
FYRSNT
VYHGSA
LYRGKE

FIG.10

YYSGRA

SYTGNM
RLSMYQ
FYVSMF
YQSVRM
SYAAAS
RTVNYG
LYEGSE
YYRSRQ
LYSTES
VYASRG
YTNSDY
IYEGRA
MYQGRH
AYRGEQ
IYSSSS
LYTDGF
AYAGGG
YYQVSN
YYQQGD
YYSKNA
FYHGNR
MYNGLG
YYADRA
FYVSEA
YYSRPV
LYTHQV
YQSSGS
LYNNEA
NYSVEV
FYADHT

FIG.11

KRGRKK

LRWRSG
SLRSKK
NVKQGV
KERLPE
DNMNSR
KKGRAV
QDTVKN
SRSNRK
KMLRKA
ASTHGK
MYGRTN

FIG.12

LNSRCN

LRWRSG
SLRSKK
NVKQGV
KERLPE
DNMNSR
KKGRAV
QDTVKN
SRSNRK
KMLRKA
ASTHGK
RDDVGN
SNNMNE
WSCCDS
KNKSRV
LFSGNE
FNSADW
RSAGLN
LDDIPA
LTLETN

FIG.13

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FIG. 14A

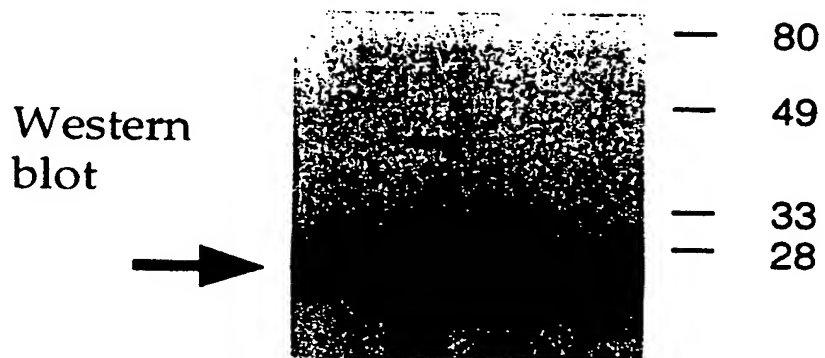


FIG. 14B

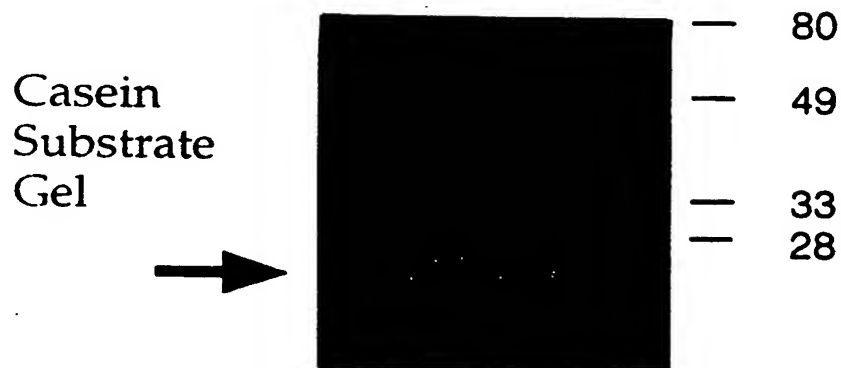


FIG. 14C

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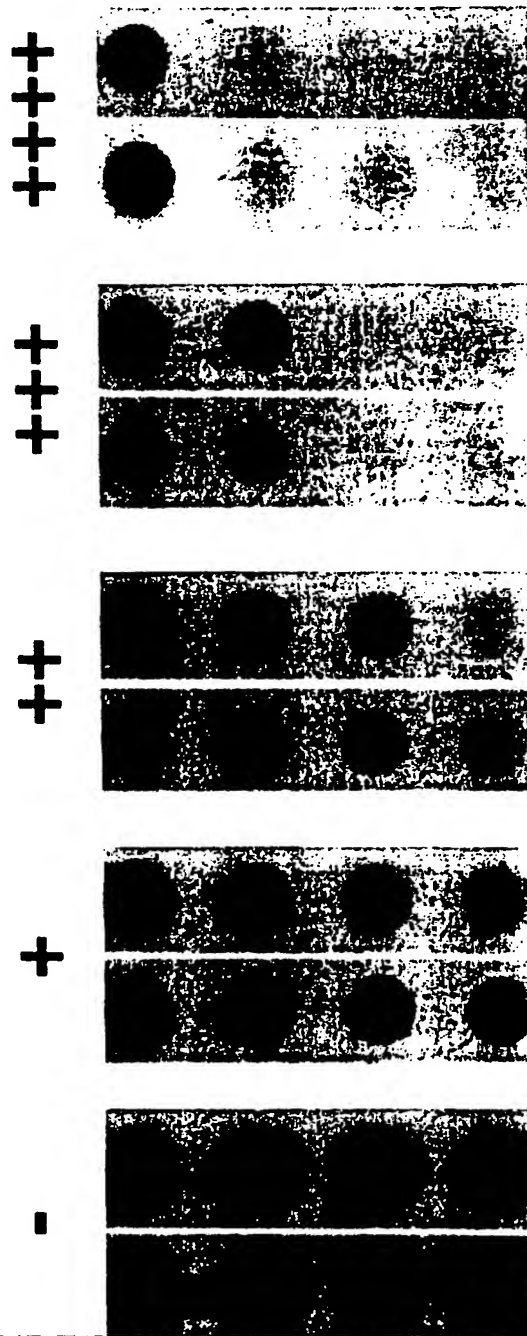


FIG. 15A FIG. 15B FIG. 15C FIG. 15D FIG. 15E

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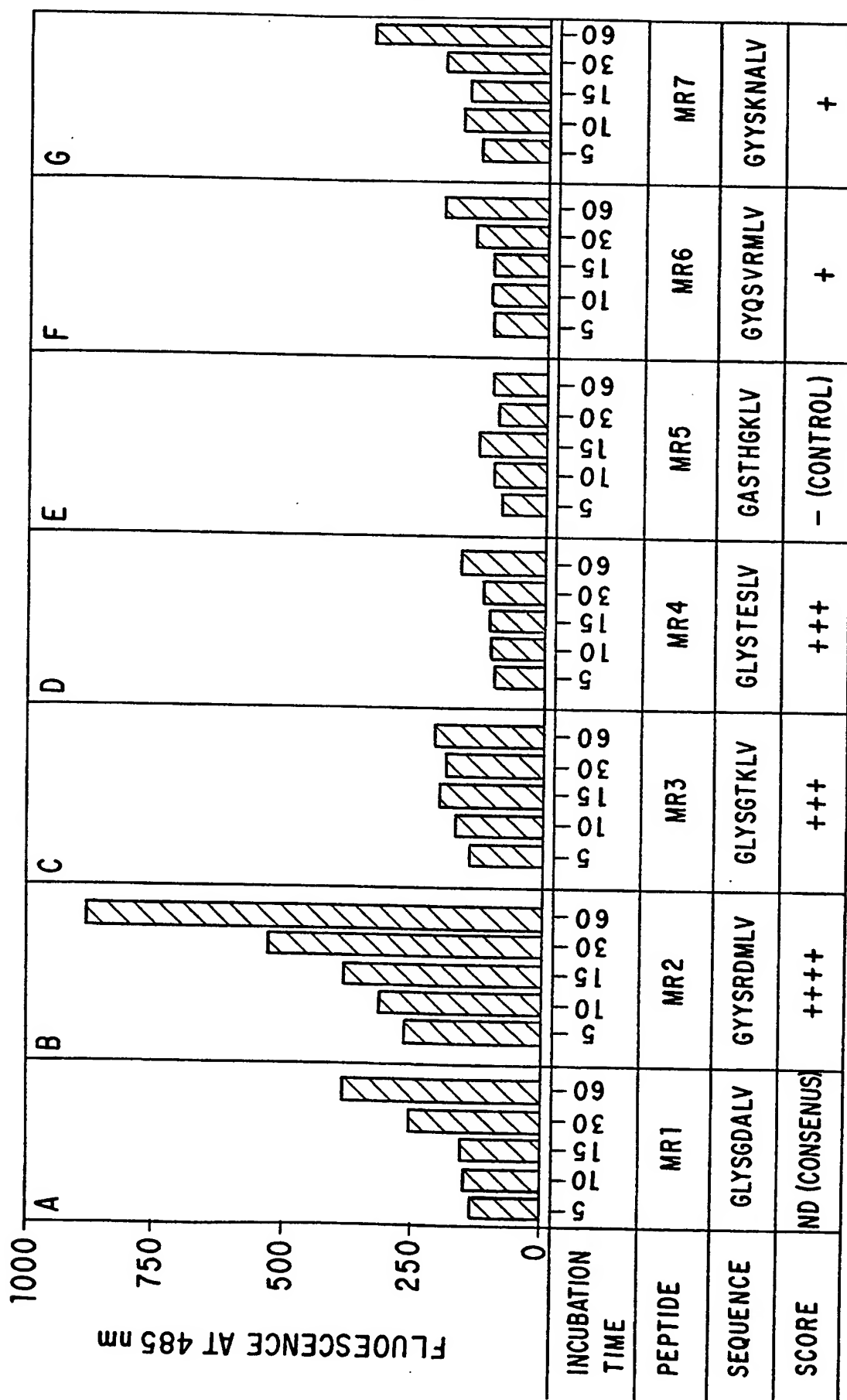


FIG. 16

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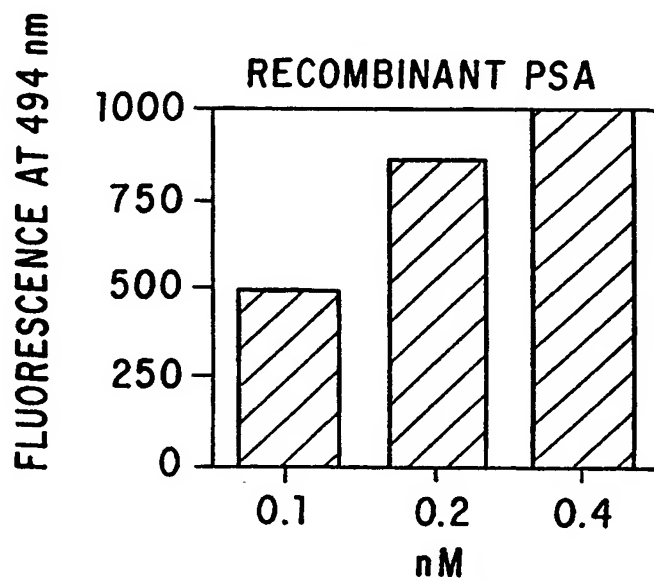


FIG. 17A

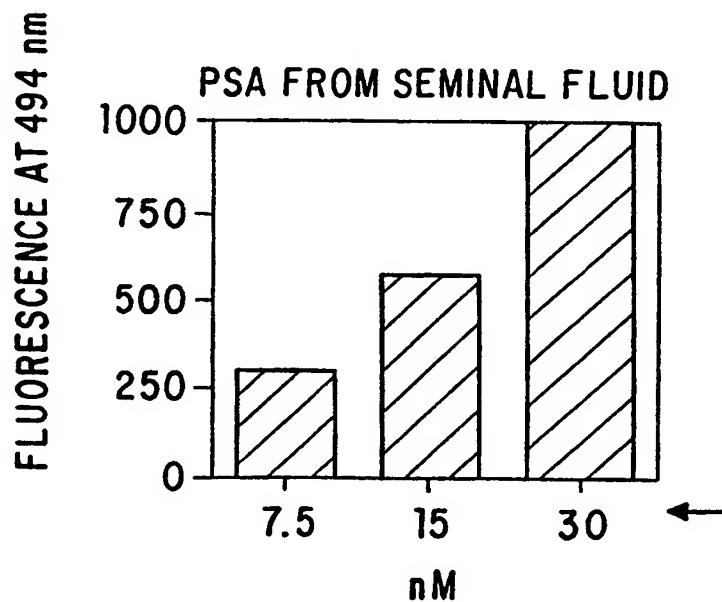


FIG. 17B

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Series B
250 $\mu\text{g/ml}$ of PSA

Consensus Sequence

LYSGSA

YYQQGD	LYEGGT
YYSKNA	RYSNGG
YYSRDM	LYKGNL
FYHGNR	FYRSDK
YYSDRK	FYSBRE
HYEGGM	SYTGNN
VYSNDK	FYVSMF
MYNGLG	LYSSDL
YYADRA	YYSDSV
VYYGGA	IYSMGN
SYSADA	-YQSTPD
LYSSST	LYSSSV
FYRSNT	VYSSDN
VYHGSA	-YQSVRM
YYEGSM	SYSATS
SYSGGN	HYGFKP
MYSADA	LYEGSE
FYVSEA	-YISVPG
LYHSDN	YYRSRQ
YYSRPV	LYSTES
LYTHQV	RYEMDV
-YQSSGS	VYASRG
NYDGGV	LYSGTK
LYRGKE	-YTAGSY
VYKGGE	-YTNSDY
LYPWFS	IYEGRA
LYNNEA	TYMGSS
NYSVEV	MYQGRH
YMAGST	FYHRHR
FYADHT	SYSDDL
HYGMDV	QYASDS
FYDSNV	AYRGDQ
PYQGGEL	LYSGKG
LYQGED	KYAADV
RYEGNA	FYTADS
FYSGEE	LYRGDD
-YQASSY	IYSSSS
NYSGRK	LYTDGF
FYAQSQ	AYAGGG
HYAANN	QYTGST
NYAGSG	YYQVSN
NYTREF	

Series C
50 $\mu\text{g/ml}$ of PSA

Consensus Sequence

YYSGEV

-YMSSDM
AYFARK
LYSREM
NYAGSG
-YRRAKR
MYTGEM
NYEMDF
HYSGGE
SYSSEY
FYEGDN
-YRKAKR
LYRSEA
YYRVNS
MYSGGE
NYSGEG
FYRTEV
FYQGDS
NYSGDV
YYKSEN
TYAGGT
YYSVSQ
MYSGRE
YYATSR
YYSGNA
VYGNSV
-YQAGGE
YYFNET
NYSGDV
WYCWHI
HYSGGE
HYSSSV
GYNKGI
FYQGSQ
HYQGGD
YYAGKD
FYQGSQ
FYQGTQ
NYDGGV
MYSAET

FIG.18

SUBSTITUTE SHEET (RULE 26)

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/04557

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) : Please See Extra Sheet.

US CL : 435/7.1, 7.4; 436/63; 514/2; 530/329, 330

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/7.1, 7.4; 436/63; 514/2; 530/329, 330

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

DIALOG, APS

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	US 5,599,686 A (DEFEO-JONES et al.) 04 February 1997, columns 2-5.	1-8, 18-27
Y	CHRISTENSSON, A. et al. Enzymatic Activity of Prostate-specific Antigen and its Reactions with Extracellular Serine Proteinase Inhibitors. European J. Biochem. 1990, Vol. 194, pages 755-763, especially page 755.	1-8, 18-27



Further documents are listed in the continuation of Box C.



See patent family annex.

* Special categories of cited documents:	*T	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
A document defining the general state of the art which is not considered to be of particular relevance	*X*	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
E earlier document published on or after the international filing date	*Y*	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*G*	document member of the same patent family
O document referring to an oral disclosure, use, exhibition or other means		
P document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search

02 JUNE 1998

Date of mailing of the international search report

20 JUL 1998

Name and mailing address of the ISA/US
Commissioner of Patents and Trademarks
Box PCT
Washington, D.C. 20231

Facsimile No. (703) 305-3230

Authorized officer

YVONNE EYLER

Telephone No. (703) 308-0196

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/04557**Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)**

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☒ Claims Nos.: 9-17
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

The claims are drawn to specific sequences for which the errors in the crf preclude searching.
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

☐
☐

The additional search fees were accompanied by the applicant's protest.

No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US98/04557

A. CLASSIFICATION OF SUBJECT MATTER:

IPC (6): G01N 33/48, 33/53, 33/573; A01N 37/18; A61K 38/00, 38/04; C07K 5/00, 7/00, 16/00, 17/00

